

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1 to 30 (canceled)

Claim 31 (previously presented): A method for cleaving a nucleic acid substrate with a nucleic acid enzyme comprising mixing said substrate with the nucleic acid enzyme of claim 44.

Claims 32 to 43 (canceled)

Claim 44 (previously presented): A nucleic acid enzyme capable of recognizing and cleaving a nucleic acid substrate, said nucleic acid enzyme which when bound to the substrate comprises:

(i) a first nucleotide sequence

5'-G¹G²G³U⁴C⁵C⁶A¹³C¹⁴C¹⁵UC¹⁶C¹⁷UCGCG¹⁵G¹⁴U¹³N¹N²N³N⁴N⁵N⁶N⁷G¹⁷G¹⁶G⁷C⁸A⁹U¹⁰G¹¹C¹²S¹B¹Y-3' (SEQ ID NO: 65); and

(ii) a second nucleotide sequence

5'-B²KS²G¹²C¹¹A¹⁰U⁹G⁸G⁷CUAAGG⁶G⁵A⁴C³C²C¹-3' (SEQ ID NO: 66);

wherein non-variable nucleotides having the same superscript form conventional Watson-Crick base pairs, except the two G⁷ form a homopurine base pair;

S¹ and S² are each independently selected from the group consisting of G and C;

B¹ and B² are each independently selected from the group consisting of G, C, U and T;

K is selected from the group consisting of G, U and T;

Y is selected from the group consisting of C, U and T;

S¹ and S² form a conventional Watson-Crick base pair;

Y and B² may form a conventional Watson-Crick base pair;

B¹ and K may form a conventional Watson-Crick base pair;

B¹, K, Y and B² may together form a loop;

N¹N²N³N⁴N⁵N⁶N⁷ forms a substrate binding region;

N¹, N², N³, N⁴, N⁵ and N⁶ are each a nucleotide which may be the same or different;

N⁷ is U;

N⁷ is capable of forming a wobble pair with the substrate;

N¹, N², N³, N⁵ and N⁶ are capable of forming conventional Watson-Crick base pairs with the substrate; and

N⁴ is capable of forming a non-conventional Watson-Crick base pair and a conventional Watson-Crick base pair.

Claim 45 (previously presented): The nucleic acid enzyme of claim 44, wherein said enzyme comprises a nucleotide sequence selected from the group consisting of:

(i) 5'-G¹G²G³U⁴C⁵C⁶A¹³C¹⁴C¹⁵UC¹⁶C¹⁷UCGCG¹⁵G¹⁴U¹³N¹N²N³N⁴N⁵N⁶N⁷G¹⁷G¹⁶G⁷C⁸A⁹U¹⁰G¹¹C¹²G¹⁸GCUUC¹⁸G¹²C¹¹A¹⁰U⁹G⁸G⁷CUAAGG⁶G⁵A⁴C³C²C¹-3',
(SEQ ID NO: 61); and

(ii) 5'-G¹G²G³U⁴C⁵C⁶A¹³C¹⁴C¹⁵UC¹⁶C¹⁷UCGCG¹⁵G¹⁴U¹³N¹N²N³N⁴N⁵N⁶N⁷G¹⁷G¹⁶G⁷C⁸A⁹U¹⁰G¹¹C¹²C¹⁸UUCGG¹⁸G¹²C¹¹A¹⁰U⁹G⁸G⁷CUAAGG⁶G⁵A⁴C³C²C¹-3',
(SEQ ID NO: 62).

Claim 46 (previously presented): The nucleic acid enzyme of claim 44, wherein said first nucleotide sequence is

5'-G¹G²G³U⁴C⁵C⁶A¹³C¹⁴C¹⁵UC¹⁶C¹⁷UCGCG¹⁵G¹⁴U¹³N¹N²N³N⁴N⁵N⁶N⁷G¹⁷G¹⁶G⁷C⁸A⁹U¹⁰G¹¹C¹²G¹⁸C¹⁹C²⁰-3' (SEQ ID NO: 63) and said second nucleotide sequence is
5'-G²⁰G¹⁹C¹⁸G¹²C¹¹A¹⁰U⁹G⁸G⁷CUAAGG⁶G⁵A⁴C³C²C¹-3' (SEQ ID NO: 64).

Claim 47 (previously presented): The nucleic acid of claim 44, wherein N¹N²N³N⁴N⁵N⁶N⁷ is selected from the group consisting of:

- (i) CCGACCU;
- (ii) CCCAGCU;
- (iii) GGGAUAU;
- (iv) CCGCCCU;
- (v) CCGGCCU;
- (vi) CCGUCCU;
- (vii) CCGAACU;
- (viii) CCGAGCU;
- (ix) CCGAUCU;
- (x) CCUCUUU;
- (xi) CCUUGUU;
- (xii) UGUUCUU;
- (xiii) GGGGUUU;
- (xiv) UCCCCUU;
- (xv) GGACUCU;
- (xvi) UCGACUU; and
- (xvii) GCCACCU.

Claim 48 (previously presented): The nucleic acid enzyme of claim 44, wherein the enzyme is derived from hepatitis delta virus.

Claims 49 and 50 (canceled)

Claim 51 (previously presented): The nucleic acid enzyme of claim 44, wherein the enzyme is composed of ribonucleotides.

Claim 52 (previously presented): The nucleic acid enzyme of claim 44, wherein the enzyme is composed of a mixture of ribonucleotides and deoxyribonucleotides.

Claim 53 to 62 (canceled)

Claim 63 (new): A nucleic acid enzyme capable of recognizing and cleaving a nucleic acid substrate, said nucleic acid enzyme which when bound to the substrate comprises:

(i) a first nucleotide sequence

5'-G¹G²G³U⁴C⁵C⁶A¹³C¹⁴C¹⁵UC¹⁶C¹⁷UCGCG¹⁵G¹⁴U¹³N¹N²N³N⁴N⁵N⁶N⁷G¹⁷G¹⁶G⁷C⁸A⁹U¹⁰G¹¹C¹²S¹B¹Y-3' (SEQ ID NO: 65); and

(ii) a second nucleotide sequence

5'-B²K³S²G¹²C¹¹A¹⁰U⁹G⁸G⁷CUAAGG⁶G⁵A⁴C³C²C¹-3' (SEQ ID NO: 66);

wherein non-variable nucleotides having the same superscript form conventional Watson-Crick base pairs, except the two G⁷ form a homopurine base pair;

S¹ and S² are each independently selected from the group consisting of G and C;

B¹ and B² are each independently selected from the group consisting of G, C, U and T;

K is selected from the group consisting of G, U and T;

Y is selected from the group consisting of C, U and T;

S¹ and S² form a conventional Watson-Crick base pair;

Y and B² may form a conventional Watson-Crick base pair;

B¹ and K may form a conventional Watson-Crick base pair;

B¹, K, Y and B² may together form a loop;

N¹N²N³N⁴N⁵N⁶N⁷ forms a substrate binding region;

N¹, N², N³, N⁴, N⁵ and N⁶ are each a nucleotide which may be the same or different;

N⁷ is U;

N⁷ is capable of forming a wobble pair with the substrate;

N¹, N², N³, N⁵ and N⁶ are capable of forming conventional Watson-Crick base pairs with the substrate; and

N⁴ is capable of forming a non-conventional Watson-Crick base pair and a conventional Watson-Crick base pair,

wherein the enzyme is incapable of forming a bond with the nucleotide residues of said substrate in positions -1 and -2 directly 5' to the cleavage site.

Claim 64 (new): The nucleic acid enzyme of claim 44, wherein G¹⁶ and G¹⁷ are incapable of forming a bond with the substrate.

Claim 65 (new): A nucleic acid enzyme capable of recognizing and cleaving a nucleic acid substrate, said nucleic acid enzyme which when bound to the substrate comprises:

(i) a first nucleotide sequence

5'-G¹G²G³U⁴C⁵C⁶A¹³C¹⁴C¹⁵UC¹⁶C¹⁷UCGCG¹⁵G¹⁴U¹³N¹N²N³N⁴N⁵N⁶N⁷G¹⁷G¹⁶G⁷C⁸A⁹U¹⁰G¹¹C¹²S¹B¹Y-3' (SEQ ID NO: 65); and

(ii) a second nucleotide sequence

5'-B²KS²G¹²C¹¹A¹⁰U⁹G⁸G⁷CUAAGG⁶G⁵A⁴C³C²C¹-3' (SEQ ID NO: 66);

wherein non-variable nucleotides having the same superscript form conventional Watson-Crick base pairs, except the two G⁷ form a homopurine base pair;

S¹ and S² are each independently selected from the group consisting of G and C;

B¹ and B² are each independently selected from the group consisting of G, C, U and T;

K is selected from the group consisting of G, U and T;

Y is selected from the group consisting of C, U and T;

S¹ and S² form a conventional Watson-Crick base pair;

Y and B² may form a conventional Watson-Crick base pair;

B¹ and K may form a conventional Watson-Crick base pair;

B¹, K, Y and B² may together form a loop;

N¹N²N³N⁴N⁵N⁶N⁷ forms a substrate binding region;

N¹, N², N³, N⁴, N⁵ and N⁶ are each a nucleotide which may be the same or different;

N⁷ is U;

N⁷ is capable of forming a wobble pair with the substrate;

N¹, N², N³, N⁵ and N⁶ are capable of forming conventional Watson-Crick base pairs with the substrate; and

N⁴ is capable of forming a non-conventional Watson-Crick base pair and a conventional Watson-Crick base pair,

wherein the enzyme is adapted to bind to the substrate such that the enzyme is incapable of interacting with nucleotide residues in the substrate at positions -1 and -2 directly 5' to the cleavage site and the enzyme is capable of forming a GU wobble pair with the nucleotide residue (G) in the substrate directly 3' to the cleavage site.